WEST Search History

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DATE: Tuesday, August 28, 2007

Hide?	Set Name	Query	Hit Count
	DB=USPT; PLUR=YES; OP=OR		
☐	L4	L2 and synapse	0
☐	L3	L2 and NMDA	0
☐	L2	L1 and memory	13
☐	L1	Prickle	2088

END OF SEARCH HISTORY

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=> d his

     (FILE 'HOME' ENTERED AT 12:46:26 ON 28 AUG 2007)

     FILE 'MEDLINE, BIOSIS, EMBASE, CAPLUS' ENTERED AT 12:46:43 ON 28 AUG 2007
L1          1499 S PRICKLE
L2             3 S L1 AND MEMOR?
L3            10 S L1 AND SYNAP?
L4             3 S L1 AND NMDA
L5             3 DUP REM L2 (0 DUPLICATES REMOVED)

=>
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<!--StartFragment-->RESULT 5
ABG07025
ID ABG07025 standard; protein; 795 AA.
XX
AC ABG07025;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #7016.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS71212.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 37384; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 795 AA;

Query Match 80.5%; Score 3675; DB 4; Length 795;
Best Local Similarity 84.9%; Pred. No. 3.3e-276;
Matches 688; Conservative 31; Mismatches 65; Indels 26; Gaps 7;

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Qy         49 VHQYYSCLPEEKVPYVNSPGEKLRIKQLLHQLPPHDNEVRYCNSLDEEEKRELKLFSNQR 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:||
Db          1 VHQYYSCLPEEKVPYVNSPGEKLRIKQLLHQLPPHDNEVRYCNSLDEEEKRELKLFSSQR 60

Qy        109 KRENLGRGNVRPFPVTMTGAICEQCGGQIKGGDIAVFASRAGHGICWHPPCFICTVCNEL 168
              |||||||||||||||||||||||||| |||||||||||||:|||||||:|||||||
Db         61 KRENLGRGNVRPFPVTMTGAICEQCGGQINGGDIAVFASRAGHGVCWHPPCFVCTVCNEL 120

Qy        169 LVDLIYFYQDGKIYCGRHHAECLKPRCAACDEIIFADECTEAEGRHWHMRHFCCFECETV 228
              ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
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Db        121 LVDLIYFYQDGKIYCGRHHAECLKPRCAACDEIIFADECTEAEGRHWHMKHFCCFECETV 180

Qy        229 LGGQRYIMKEGRPYCCHCFESLYAEYCDTCAQHIGIDQGQMTYDGQHWHATENCFCCAHC 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        181 LGGQRYIMKEGRPYCCHCFESLYAEYCDTCAQHIGIDQGQMTYDGQHWHATETCFCCAHC 240

Qy        289 KKSLLGRPFLPKQGQIFCSRACSAGEDPNGSDSSDSAFQNARAKESRRSAKIGK---NKG 345
              ||||||||||||||||||||||||||||||||||||||  :      |: :    :|
Db        241 KKSLLGRPFLPKQGQIFCSRACSAGEDPNGSDSSDSAFQNAGPRSPGAVPKLARTRARRG 300

Qy        346 KTEETMLNQHSQLQVSSNR----LSADVDPLSVQMDLLSLSSQTPSLNRD----PIWRSR 397
                 |      |:   : :|    ::||     || |  :     | |       |:|
Db        301 AHAEPAQPAASEFXPAVSRRRPPVTADGHAQPVQPD--TQPQPGPHLEEPGRALPLWEQD 358

Qy        398 DEPFHYGNKMEQNQSQSPLQLLSQCNIRTSYSPGGQAAGAQPDMWAKHFSNPKRSSSMAL 457
                    | : :   | :|     |||||||||||| |||||:|| ||||||||||:|:
Db        359 ------GAEPDPEPSAAP----RQCNIRTSYSPGGQGAGAQPEMWGKHFSNPKRSSSLAM 408

Qy        458 KGHGGSFIQECREDYYPGRLMSQESYSDMSSQSFSETRGSIPVPKYEEEEEEEEEGGIS 517
               || ||||:|||||||||| |||||||||||||||||| ||||   |||||||||:|
Db        409 TGHAGSFIKECREDYYPGRLRSQESYSDMSSQSFSETRGSIQVPKY---EEEEEEGGLS 465

Qy        518 TQQCRPRRPLSSLKYTEDMTPTEQTPRGSMESLALSNATGLSAEGGAKRQEHLSRFSMPD 577
              ||||| | |:||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        466 TQQCRTRHPISSLKYTEDMTPTEQTPRGSMESLALSNATGLSADGGAKRQEHLSRFSMPD 525

Qy        578 LSKDSGMNVSEKLSNMGTLNSSMQFRSAESVRSLLSAQQYQEMEGNLHQLSNPLGYRDLQ 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        526 LSKDSGMNVSEKLSNMGTLNSSMQFRSAESVRSLLSAQQYQEMEGNLHQLSNPIGYRDLQ 585

Qy        638 SHGRMHQSFDFDGGIASSKLPGQEGVHIQPMSERTRRRTTSRDDNRRFRPHRSRRSRRSR 697
              ||||||||||||||:| |||||||| |||||||||| |||||||||||||||||||||||
Db        586 SHGRMHQSFDFDGGMAGSKLPGQEGVRIQPMSERTRRRATSRDDNRRFRPHRSRRSRRSR 645

Qy        698 SDNALHLASEREVIARLKDRPPLRAREDYDQFVRQRSFQESMGQGSRRDLYSQCPRTVSD 757
              |||||||||||| |:||||||||||||||||:|||||||||| ||||||| ||||||||
Db        646 SDNALHLASEREAISRLKDRPPLRAREDYDQFMRQRSFQESMGHGSRRDLYGQCPRTVSD 705

Qy        758 LALQNAFGERWGPYFTEYDWCSTCSSSSESDNEGYFLGEPIPQPARLRYVTSDELLHKYS 817
              ||||||||:|||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        706 LALQNAFGDRWGPYFAEYDWCSTCSSSSESDNEGYFLGEPIPQPARLRYVTSDELLHKYS 765

Qy        818 SYGVPKSSTLGGRGQLHSRKRQKSKNCIIS 847
              |||:||||||||||||||||||||||||||
Db        766 SYGLPKSSTLGGRGQLHSRKRQKSKNCIIS 795
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<!--EndFragment-->